



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:04 PM UTC

PDB ID : 2QA0 / pdb\_00002qa0  
Title : Structure of Adeno-Associated virus serotype 8  
Authors : Nam, H.-J.  
Deposited on : 2007-06-14  
Resolution : 2.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

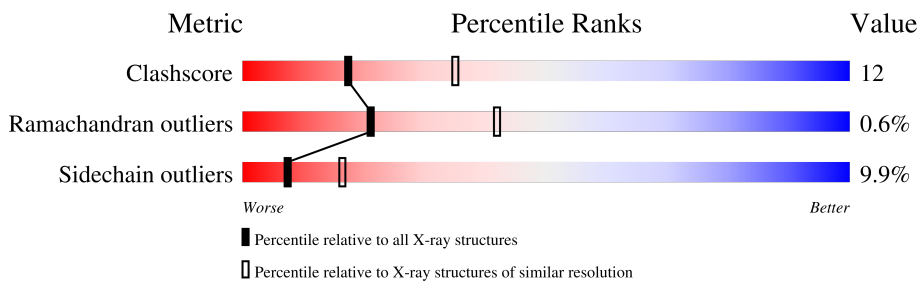
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	519	 73% 22% 5%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4226 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	519	4136	2609	716	798	13	0	0	0

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Na	0	0
			1	1		

- Molecule 3 is water.

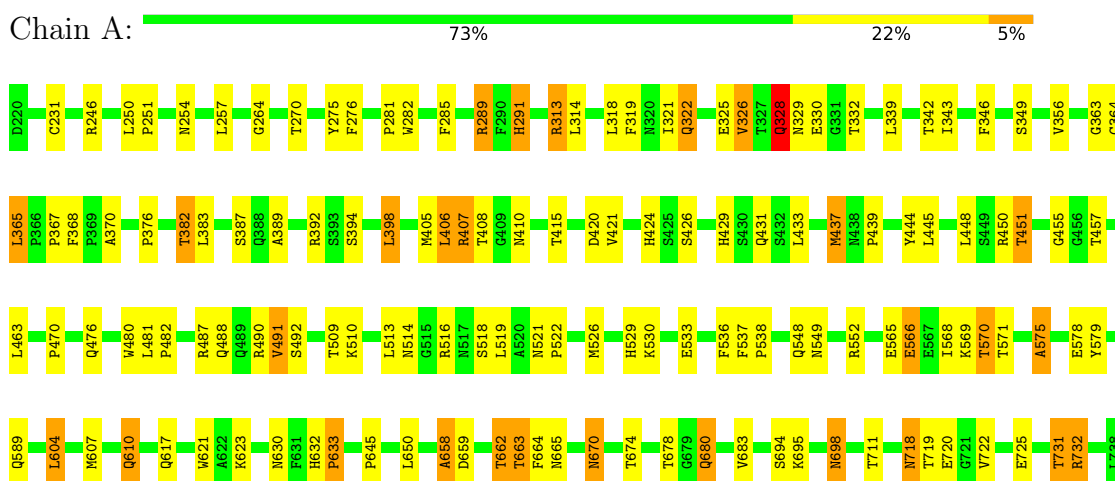
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	89	Total	O	0	0
			89	89		

### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

- Molecule 1: Capsid protein



## 4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	254.84Å 254.84Å 445.43Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.00 – 2.60	Depositor
% Data completeness (in resolution range)	78.1 (40.00-2.60)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.11	Depositor
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.255 , 0.259	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	4226	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	34.0	wwPDB-VP

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section:  
NA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.51	0/4259	1.06	22/5811 (0.4%)

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	328	GLN	OE1-CD-NE2	-10.53	112.07	122.60
1	A	365	LEU	CA-C-N	7.49	125.12	119.66
1	A	365	LEU	C-N-CA	7.49	125.12	119.66
1	A	328	GLN	CG-CD-NE2	7.33	127.39	116.40
1	A	579	TYR	N-CA-C	-6.95	103.14	111.69
1	A	632	HIS	CA-C-N	6.76	128.29	119.84
1	A	632	HIS	C-N-CA	6.76	128.29	119.84
1	A	444	TYR	N-CA-C	-6.75	105.04	113.28
1	A	719	THR	N-CA-C	-6.71	104.95	113.01
1	A	732	ARG	N-CA-C	6.63	120.24	108.24
1	A	664	PHE	N-CA-C	6.24	119.04	110.24
1	A	694	SER	N-CA-C	6.04	119.74	110.20
1	A	408	THR	CA-C-N	-5.47	116.93	123.44
1	A	408	THR	C-N-CA	-5.47	116.93	123.44
1	A	725	GLU	CA-C-N	5.45	125.28	119.28
1	A	725	GLU	C-N-CA	5.45	125.28	119.28
1	A	575	ALA	N-CA-C	5.42	118.99	112.38
1	A	407	ARG	N-CA-C	-5.28	102.64	110.46
1	A	480	TRP	N-CA-C	5.19	117.30	109.41
1	A	658	ALA	N-CA-C	-5.16	103.88	110.53
1	A	665	ASN	CA-C-N	5.03	127.33	120.54
1	A	665	ASN	C-N-CA	5.03	127.33	120.54

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4136	0	3893	100	0
2	A	1	0	0	0	0
3	A	89	0	0	5	0
All	All	4226	0	3893	100	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (100) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:382:THR:HG21	1:A:394:SER:H	1.05	1.11
1:A:289:ARG:HG2	1:A:289:ARG:HH11	0.95	1.08
1:A:289:ARG:HG2	1:A:289:ARG:NH1	1.71	1.00
1:A:289:ARG:HH11	1:A:289:ARG:CG	1.82	0.90
1:A:382:THR:HG21	1:A:394:SER:N	1.88	0.87
1:A:426:SER:HA	1:A:731:THR:HG23	1.60	0.81
1:A:718:ASN:HB3	1:A:720:GLU:H	1.46	0.79
1:A:429:HIS:HB2	1:A:570:THR:HG21	1.67	0.77
1:A:566:GLU:O	1:A:569:LYS:HG3	1.86	0.74
1:A:437:MET:O	1:A:439:PRO:HD3	1.88	0.74
1:A:363:GLY:HA3	1:A:376:PRO:HG3	1.71	0.73
1:A:406:LEU:N	1:A:406:LEU:HD23	2.07	0.70
1:A:289:ARG:NH1	1:A:617:GLN:O	2.25	0.70
1:A:426:SER:HA	1:A:731:THR:CG2	2.23	0.68
1:A:698:ASN:HD22	1:A:698:ASN:H	1.39	0.68
1:A:405:MET:C	1:A:406:LEU:HD23	2.23	0.63
1:A:330:GLU:C	1:A:332:THR:H	2.06	0.63
1:A:630:ASN:OD1	1:A:633:PRO:HG3	1.99	0.63
1:A:321:ILE:HD13	1:A:343:ILE:HD11	1.82	0.62
1:A:322:GLN:HG3	1:A:678:THR:HG23	1.82	0.62
1:A:264:GLY:HA3	1:A:387:SER:HB3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:439:PRO:O	1:A:470:PRO:HB3	2.00	0.61
1:A:322:GLN:NE2	3:A:792:HOH:O	2.32	0.61
1:A:623:LYS:HB2	1:A:645:PRO:HG3	1.83	0.61
1:A:383:LEU:HD12	1:A:392:ARG:HB2	1.84	0.60
1:A:718:ASN:HB2	1:A:722:VAL:H	1.67	0.60
1:A:314:LEU:C	1:A:314:LEU:HD12	2.27	0.59
1:A:367:PRO:HD2	3:A:782:HOH:O	2.02	0.59
1:A:426:SER:CA	1:A:731:THR:HG23	2.31	0.59
1:A:313:ARG:HH11	1:A:313:ARG:HB3	1.68	0.58
1:A:270:THR:HG22	3:A:790:HOH:O	2.03	0.57
1:A:398:LEU:CD1	1:A:650:LEU:HD22	2.34	0.57
1:A:264:GLY:CA	1:A:387:SER:HB3	2.34	0.56
1:A:658:ALA:O	1:A:659:ASP:C	2.48	0.56
1:A:451:THR:HG23	3:A:753:HOH:O	2.06	0.56
1:A:698:ASN:H	1:A:698:ASN:ND2	2.00	0.56
1:A:285:PHE:CZ	1:A:318:LEU:HD21	2.41	0.56
1:A:424:HIS:CD2	1:A:731:THR:HG21	2.41	0.55
1:A:382:THR:CG2	1:A:394:SER:H	1.98	0.55
1:A:328:GLN:HA	1:A:328:GLN:OE1	2.06	0.55
1:A:406:LEU:HB3	1:A:410:ASN:HB2	1.90	0.54
1:A:565:GLU:O	1:A:568:ILE:HG12	2.08	0.53
1:A:529:HIS:HD2	1:A:530:LYS:O	1.91	0.53
1:A:326:VAL:HG13	1:A:674:THR:HG22	1.92	0.52
1:A:426:SER:CB	1:A:731:THR:HG23	2.41	0.51
1:A:570:THR:HG23	1:A:571:THR:HG23	1.93	0.51
1:A:289:ARG:NH1	1:A:289:ARG:CG	2.53	0.50
1:A:533:GLU:HB3	1:A:536:PHE:HD1	1.77	0.49
1:A:510:LYS:HB3	1:A:518:SER:O	2.12	0.49
1:A:313:ARG:HB3	1:A:313:ARG:NH1	2.28	0.49
1:A:346:PHE:CZ	1:A:650:LEU:HD13	2.48	0.49
1:A:457:THR:HG22	1:A:457:THR:O	2.13	0.49
1:A:731:THR:HG22	1:A:732:ARG:HG3	1.95	0.49
1:A:491:VAL:HG22	1:A:537:PHE:CE2	2.47	0.48
1:A:291:HIS:CD2	1:A:367:PRO:HG3	2.49	0.48
1:A:568:ILE:C	1:A:570:THR:N	2.72	0.47
1:A:382:THR:HG22	1:A:383:LEU:H	1.79	0.47
1:A:514:ASN:O	1:A:514:ASN:CG	2.54	0.47
1:A:680:GLN:NE2	3:A:765:HOH:O	2.47	0.47
1:A:437:MET:O	1:A:439:PRO:CD	2.62	0.46
1:A:246:ARG:HG3	1:A:365:LEU:HB3	1.98	0.45
1:A:610:GLN:HE21	1:A:610:GLN:CA	2.28	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:437:MET:HG2	1:A:476:GLN:OE1	2.16	0.45
1:A:526:MET:HB2	1:A:575:ALA:HB2	1.99	0.45
1:A:275:TYR:CD1	1:A:275:TYR:C	2.95	0.44
1:A:488:GLN:HA	1:A:509:THR:OG1	2.17	0.44
1:A:330:GLU:CD	1:A:330:GLU:N	2.75	0.44
1:A:670:ASN:H	1:A:670:ASN:HD22	1.66	0.44
1:A:695:LYS:HA	1:A:695:LYS:HD2	1.88	0.44
1:A:492:SER:HB2	1:A:536:PHE:CE2	2.53	0.44
1:A:568:ILE:C	1:A:570:THR:H	2.25	0.43
1:A:321:ILE:HD13	1:A:343:ILE:CD1	2.46	0.43
1:A:329:ASN:O	1:A:332:THR:HB	2.18	0.43
1:A:398:LEU:N	1:A:398:LEU:HD23	2.34	0.43
1:A:538:PRO:HG3	1:A:575:ALA:HB3	2.01	0.43
1:A:291:HIS:CE1	1:A:367:PRO:HG3	2.54	0.43
1:A:604:LEU:O	1:A:607:MET:HG3	2.18	0.43
1:A:450:ARG:HH11	1:A:450:ARG:HG3	1.83	0.43
1:A:670:ASN:HD22	1:A:670:ASN:C	2.26	0.42
1:A:276:PHE:CZ	1:A:389:ALA:HB2	2.53	0.42
1:A:291:HIS:NE2	1:A:367:PRO:HG3	2.35	0.42
1:A:533:GLU:HB3	1:A:536:PHE:CD1	2.54	0.42
1:A:282:TRP:NE1	1:A:398:LEU:HB2	2.35	0.42
1:A:406:LEU:HB3	1:A:410:ASN:CB	2.48	0.42
1:A:289:ARG:HD2	1:A:364:CYS:SG	2.59	0.42
1:A:552:ARG:O	1:A:552:ARG:HG2	2.19	0.42
1:A:662:THR:HG22	1:A:663:THR:HG22	2.01	0.42
1:A:482:PRO:O	1:A:607:MET:HE2	2.20	0.42
1:A:250:LEU:HD12	1:A:251:PRO:HD2	2.01	0.42
1:A:257:LEU:O	1:A:281:PRO:HG3	2.19	0.42
1:A:342:THR:HG22	1:A:407:ARG:HG2	2.01	0.41
1:A:431:GLN:O	1:A:570:THR:OG1	2.38	0.41
1:A:424:HIS:NE2	1:A:731:THR:HG21	2.35	0.41
1:A:521:ASN:HA	1:A:522:PRO:HA	1.78	0.41
1:A:621:TRP:CD1	1:A:621:TRP:C	2.98	0.41
1:A:254:ASN:HB3	1:A:257:LEU:O	2.20	0.41
1:A:319:PHE:CD2	1:A:319:PHE:N	2.88	0.41
1:A:330:GLU:C	1:A:332:THR:N	2.74	0.41
1:A:490:ARG:HD2	1:A:536:PHE:CG	2.56	0.41
1:A:368:PHE:CE2	1:A:370:ALA:HB3	2.56	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	517/519 (100%)	499 (96%)	15 (3%)	3 (1%)	21	42

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	455	GLY
1	A	339	LEU
1	A	633	PRO

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	453/453 (100%)	408 (90%)	45 (10%)	7	16

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	231	CYS
1	A	289	ARG
1	A	291	HIS
1	A	313	ARG
1	A	322	GLN
1	A	325	GLU
1	A	326	VAL
1	A	328	GLN

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Mol	Chain	Res	Type
1	A	349	SER
1	A	356	VAL
1	A	382	THR
1	A	398	LEU
1	A	406	LEU
1	A	415	THR
1	A	420	ASP
1	A	421	VAL
1	A	433	LEU
1	A	437	MET
1	A	445	LEU
1	A	448	LEU
1	A	451	THR
1	A	463	LEU
1	A	481	LEU
1	A	487	ARG
1	A	491	VAL
1	A	513	LEU
1	A	516	ARG
1	A	519	LEU
1	A	548	GLN
1	A	549	ASN
1	A	566	GLU
1	A	570	THR
1	A	578	GLU
1	A	589	GLN
1	A	604	LEU
1	A	610	GLN
1	A	662	THR
1	A	663	THR
1	A	670	ASN
1	A	680	GLN
1	A	683	VAL
1	A	698	ASN
1	A	711	THR
1	A	718	ASN
1	A	731	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	254	ASN

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Mol	Chain	Res	Type
1	A	263	ASN
1	A	273	ASN
1	A	322	GLN
1	A	338	ASN
1	A	361	HIS
1	A	377	GLN
1	A	429	HIS
1	A	467	GLN
1	A	529	HIS
1	A	549	ASN
1	A	601	GLN
1	A	610	GLN
1	A	644	HIS
1	A	653	ASN
1	A	665	ASN
1	A	666	GLN
1	A	670	ASN
1	A	675	GLN
1	A	680	GLN
1	A	698	ASN
1	A	718	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

### 6.4 Ligands

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers

EDS was not executed - this section is therefore empty.